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Page 1 of 7

1634

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/628,495D

DATE: 05/21/2002

TIME: 10:29:18

Input Set : A:\EP.txt

Output Set: N:\CRF3\05212002\I628495D.raw

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3 <110> APPLICANT: White, David
5 <120> TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR PROGNOSTICATION,
DIAGNOSIS,

6 PREVENTION, AND TREATMENT OF BONE-RELATED DISORDERS AND OTHER DISORDERS

8 <130> FILE REFERENCE: 10147-16U1

10 <140> CURRENT APPLICATION NUMBER: US 09/628,495D

11 <141> CURRENT FILING DATE: 2000-07-28

13 <150> PRIOR APPLICATION NUMBER: US 60/146,614

14 <151> PRIOR FILING DATE: 1999-07-30

16 <160> NUMBER OF SEQ ID NOS: 9

18 <170> SOFTWARE: PatentIn version 3.1

20 <210> SEQ ID NO: 1

21 <211> LENGTH: 613

22 <212> TYPE: PRT

23 <213> ORGANISM: Homo sapiens

25 <400> SEQUENCE: 1

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28 1 5 10 15

31 Lys Leu Pro Gln Pro Glu Tyr Pro Pro Ala Leu Ile Ile Phe Met Phe

32 20 25 30

35 Cys Ala Met Val Ile Thr Ile Val Val Asp Leu Ile Gly Asn Ser Met

36 35 40 45

39 Val Ile Leu Ala Val Thr Lys Asn Lys Lys Leu Arg Asn Ser Gly Asn

40 50 55 60

43 Ile Phe Val Val Ser Leu Ser Val Ala Asp Met Leu Val Ala Ile Tyr

44 65 70 75 80

47 Pro Tyr Pro Leu Met Leu His Ala Met Ser Ile Gly Gly Trp Asp Leu

48 85 90 95

51 Ser Gln Leu Gln Cys Gln Met Val Gly Phe Ile Thr Gly Leu Ser Val

52 100 105 110

55 Val Gly Ser Ile Phe Asn Ile Val Ala Ile Ala Ile Asn Arg Tyr Cys

56 115 120 125

59 Tyr Ile Cys His Ser Leu Gln Tyr Glu Arg Ile Phe Ser Val Arg Asn

60 130 135 140

63 Thr Cys Ile Tyr Leu Val Ile Thr Trp Ile Met Thr Val Leu Ala Val

64 145 150 155 160

67 Leu Pro Asn Met Tyr Ile Gly Thr Ile Glu Tyr Asp Pro Arg Thr Tyr

68 165 170 175

71 Thr Cys Ile Phe Asn Tyr Leu Asn Asn Pro Val Phe Thr Val Thr Ile

72 180 185 190

75 Val Cys Ile His Phe Val Leu Pro Leu Leu Ile Val Gly Phe Cys Tyr

76 195 200 205

79 Val Arg Ile Trp Thr Lys Val Leu Ala Ala Arg Asp Pro Ala Gly Gln

80 210 215 220

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84 225                230                235                240
87 Val Ile Phe Leu Leu Phe Ala Val Cys Trp Cys Pro Ile Asn Val Leu
88                245                250                255
91 Thr Val Leu Val Ala Val Ser Pro Lys Glu Met Ala Gly Lys Ile Pro
92                260                265                270
95 Asn Trp Leu Tyr Leu Ala Ala Tyr Phe Ile Ala Tyr Phe Asn Ser Cys
96                275                280                285
99 Leu Asn Ala Val Ile Tyr Gly Leu Leu Asn Glu Asn Phe Arg Arg Glu
100                290                295                300
103 Tyr Trp Thr Ile Phe His Ala Met Arg His Pro Ile Ile Phe Phe Pro
104 305                310                315                320
107 Gly Leu Ile Ser Asp Ile Arg Glu Met Gln Glu Ala Arg Thr Leu Ala
108                325                330                335
111 Arg Ala Arg Ala His Ala Arg Asp Gln Ala Arg Glu Gln Asp Arg Ala
112                340                345                350
115 His Ala Cys Pro Ala Val Glu Glu Thr Pro Met Asn Val Arg Asn Val
116                355                360                365
119 Pro Leu Pro Gly Asp Ala Ala Ala Gly His Pro Asp Arg Ala Ser Gly
120                370                375                380
123 His Pro Lys Pro His Ser Arg Ser Ser Ser Ala Tyr Arg Lys Ser Ala
124 385                390                395                400
127 Ser Thr His His Lys Ser Val Phe Ser His Ser Lys Ala Ala Ser Gly
128                405                410                415
131 His Leu Lys Pro Val Ser Gly His Ser Lys Pro Ala Ser Gly His Pro
132                420                425                430
135 Lys Ser Ala Thr Val Tyr Pro Lys Pro Ala Ser Val His Phe Lys Gly
136                435                440                445
139 Asp Ser Val His Phe Lys Gly Asp Ser Val His Phe Lys Pro Asp Ser
140                450                455                460
143 Val His Phe Lys Pro Ala Ser Ser Asn Pro Lys Pro Ile Thr Gly His
144 465                470                475                480
147 His Val Ser Ala Gly Ser His Ser Lys Ser Ala Phe Ser Ala Ala Thr
148                485                490                495
151 Ser His Pro Lys Pro Ile Lys Pro Ala Thr Ser His Ala Glu Pro Thr
152                500                505                510
155 Thr Ala Asp Tyr Pro Lys Pro Ala Thr Thr Ser His Pro Lys Pro Ala
156                515                520                525
159 Ala Ala Asp Asn Pro Glu Leu Ser Ala Ser His Cys Pro Glu Ile Pro
160                530                535                540
163 Ala Ile Ala His Pro Val Ser Asp Asp Ser Asp Leu Pro Glu Ser Ala
164 545                550                555                560
167 Ser Ser Pro Ala Ala Gly Pro Thr Lys Pro Ala Ala Ser Gln Leu Glu
168                565                570                575
171 Ser Asp Thr Ile Ala Asp Leu Pro Asp Pro Thr Val Val Thr Thr Ser
172                580                585                590
175 Thr Asn Asp Tyr His Asp Val Val Val Val Asp Val Glu Asp Asp Pro
176                595                600                605
179 Asp Glu Met Ala Val

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185 <212> TYPE: DNA
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188 <400> SEQUENCE: 2
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193 ctaccccagc cagaataccc accggctcta atcatcttta tgttctgcgc gatggttata      180
195 accatcggtg tagacctaat cggcaactcc atggtcattt tggctgtgac gaagaacaag      240
197 aagctccgga attctggcaa catcttcgtg gtcagtctct ctgtggccga tatgctggty      300
199 gccatctacc catacccttt gatgctgcat gccatgtcca ttgggggctg ggatctgagc      360
201 cagttacagt gccagatggt cgggttcata acagggctga gtgtggtcgy ctccatcttc      420
203 aacatcggtg caatcgctat caaccgttac tgctacatct gccacagcct ccagtacgaa      480
205 cggatcttca gtgtgcgcaa tacctgcata tacctggtea tcacctggat catgaccgtc      540
207 ctggctgtcc tgcccaacat gtacattggc accatcgagt acgatcctcg cacctacacc      600
209 tgcatcttca actatctgaa caaccctgtc ttactgttta ccacgtctg catccacttc      660
211 gtctctccct tctcatcgtg gggtttctgc tacgtgagga tctggaccaaa agtgcctggc      720
213 gcccgtagcc ctgcagggca gaatcctgac aaccaacttg ctgaggttcy caattttcta      780
215 accatgtttg tgatcttctt cctctttgca gtgtgctggt gccctatcaa cgtgctcact      840
217 gtcttggtgg ctgtcagtcg gaaggagatg gcaggcaaga tccccaaactg gctttatctt      900
219 gcagcctaact tcatagccta ctccaacagc tgcccaacg ctgtgatcta cgggctcttc      960
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227 gtggaggaaa ccccgatgaa tgtccggaat gtccattac ctggtgatgc tgcagctggc      1200
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231 aaatctgcct ctaccacca caagtctgtc tttagccact ccaagctgc ctctggtcac      1320
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239 actggccacc atgtctctgc tggcagccac tccaagctgc ccttcagtgc tgccaccagc      1560
241 caccctaaac ccataaagc agctaccagc catgctgagc ccaccactgc tgactatccc      1620
243 aagcctgcca ctaccagcca ccctaagccc gctgctgctg acaaccctga gctctctgcc      1680
245 tcccatgccc ccgagatccc tgccattgcc caccctgtgt ctgacgacag tgacctccct      1740
247 agctcggcct ctagccctgc cgtcgggccc accaagcctg ctgccagcca gctggagtct      1800
249 gacaccatcg ctgaccttcc tgacctact gtagtcaata ccagtaccaa tgattaccat      1860
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253 tcttaggtgg ccaggcagt                                1939
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257 <211> LENGTH: 591
258 <212> TYPE: PRT
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261 <400> SEQUENCE: 3
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267 Thr Pro Phe Gly Cys Ile Gly Cys Lys Leu Pro Lys Pro Asp Tyr Pro
268      20      25      30
271 Pro Ala Leu Ile Ile Phe Met Phe Cys Ala Met Val Ile Thr Val Val

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272          35          40          45
275 Val Asp Leu Ile Gly Asn Ser Met Val Ile Leu Ala Val Thr Lys Asn
276          50          55          60
279 Lys Lys Leu Arg Asn Ser Gly Asn Ile Phe Val Ala Ser Leu Ser Val
280 65          70          75          80
283 Ala Asp Met Leu Val Ala Ile Tyr Pro Tyr Pro Leu Met Leu Tyr Ala
284          85          90          95
287 Met Ser Val Gly Gly Trp Asp Leu Ser Gln Leu Gln Cys Gln Met Val
288          100          105          110
291 Gly Leu Val Thr Gly Leu Ser Val Val Gly Ser Ile Phe Asn Ile Thr
292          115          120          125
295 Ala Ile Ala Ile Asn Arg Tyr Cys Tyr Ile Cys His Ser Leu Gln Tyr
296          130          135          140
299 Lys Arg Ile Phe Ser Leu Arg Asn Thr Cys Ile Tyr Leu Val Val Thr
300 145          150          155          160
303 Trp Val Met Thr Val Leu Ala Val Leu Pro Asn Met Tyr Ile Gly Thr
304          165          170          175
307 Ile Glu Tyr Asp Pro Arg Thr Tyr Thr Cys Ile Phe Asn Tyr Val Asn
308          180          185          190
311 Asn Pro Ala Phe Thr Val Thr Ile Val Cys Ile His Phe Val Leu Pro
312          195          200          205
315 Leu Ile Ile Val Gly Tyr Cys Tyr Thr Lys Ile Trp Ile Lys Val Leu
316          210          215          220
319 Ala Ala Arg Asp Pro Ala Gly Gln Asn Pro Asp Asn Gln Phe Ala Glu
320 225          230          235          240
323 Val Arg Asn Phe Leu Thr Met Phe Val Ile Phe Leu Leu Phe Ala Val
324          245          250          255
327 Cys Trp Cys Pro Val Asn Val Leu Thr Val Leu Val Ala Val Ile Pro
328          260          265          270
331 Lys Glu Met Ala Gly Lys Ile Pro Asn Trp Leu Tyr Leu Ala Ala Tyr
332          275          280          285
335 Cys Ile Ala Tyr Phe Asn Ser Cys Leu Asn Ala Ile Ile Tyr Gly Ile
336          290          295          300
339 Leu Asn Glu Ser Phe Arg Arg Glu Tyr Trp Thr Ile Phe His Ala Met
340 305          310          315          320
343 Arg His Pro Ile Leu Phe Ile Ser His Leu Ile Ser Asp Ile Arg Glu
344          325          330          335
347 Thr Trp Glu Thr Arg Ala Leu Thr Arg Ala Arg Val Arg Ala Arg Asp
348          340          345          350
351 Gln Val Arg Glu Gln Glu Arg Ala Arg Ala Cys Val Ala Val Glu Gly
352          355          360          365
355 Thr Pro Arg Asn Val Arg Asn Val Leu Leu Pro Gly Asp Ala Ser Ala
356          370          375          380
359 Pro His Ser Asp Arg Ala Ser Val Arg Pro Lys Pro Gln Thr Arg Ser
360 385          390          395          400
363 Thr Ser Val Tyr Arg Lys Pro Ala Ser Ile His His Lys Ser Ile Ser
364          405          410          415
367 Gly His Pro Lys Ser Ala Ser Val Tyr Pro Lys Pro Ala Ser Ser Val
368          420          425          430

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371 His Cys Lys Pro Ala Ser Val His Phe Lys Pro Ala Ser Val His Phe
372          435          440          445
375 Lys Gly Asp Ser Val Tyr Phe Lys Gly Asp Thr Val His Tyr Arg Ala
376          450          455          460
379 Ala Ser Lys Leu Val Thr Ser His Arg Ile Ser Ala Gly Pro Ser Thr
380 465          470          475          480
383 Ser His Pro Thr Ser Met Ala Gly Tyr Ile Lys Ser Gly Thr Ser His
384          485          490          495
387 Pro Ala Thr Thr Thr Val Asp Tyr Leu Glu Pro Ala Thr Thr Ser His
388          500          505          510
391 Ser Val Leu Thr Ala Val Asp Leu Pro Glu Val Ser Ala Ser His Cys
392          515          520          525
395 Leu Glu Met Thr Ser Thr Gly His Leu Arg Ala Asp Ile Ser Ala Ser
396          530          535          540
399 Val Leu Pro Ser Val Pro Phe Glu Leu Ala Ala Thr Pro Pro Asp Thr
400 545          550          555          560
403 Thr Ala Ile Pro Ile Ala Ser Gly Asp Tyr Arg Lys Val Val Leu Ile
404          565          570          575
407 Asp Asp Asp Ser Asp Asp Ser Asp Cys Ser Asp Glu Met Ala Val
408          580          585          590

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411 <210> SEQ ID NO: 4

412 <211> LENGTH: 1800

413 <212> TYPE: DNA

414 <213> ORGANISM: Mus sp.

416 <400> SEQUENCE: 4

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VERIFICATION SUMMARY

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